

60 \*

TGTGGGTTCT AATTTACCC ACCACAAGTT TTGTCCCTACC ATAAATTGGGA TAAGGAGTCT

120 \*

AAATTCCCTT GTACAAATTTT CCAATTCTT CCTCCGCCAC ACCATATATA TACTGTACGC

180 \*

CACTTCGAAC GGTACAATGT TTGAAAAAG ACGCAGATTT TACAAAGACG GAGAAGATAA

TTAAGCTTCAA GTACTCCGAT CGTCAGGTGG CCTTTGGAAG CCAACAAACT GGCT ATG Met

240 \*

CGCT	CTT	TCT	CTT	CAC	ACT	GTA	TTT	CTC	TGC	AAA	GAG	GAA	GCC	CTC	AAT
Ala	Leu	Ser	Leu	His	Thr	Val	Phe	Leu	Cys	Lys	Glu	Glu	Ala	Leu	Asn

300 \*

Leu Tyr Ala Arg Ser Pro Cys Asn Glu Arg Phe His Arg Ser Gly Gln  
Leu Tyr Ala Arg Ser Pro Cys Asn Glu Arg Phe His Arg Ser Gly Gln  
TAT GCA AGA TCA CCA TGT AAT GAA AGG TTT CAC AGG AGT GGA CAA  
TTTA

360 \*

CCCT CCT ACC AAC ATA ATC ATG AAA ATT CGA TCC AAC AAT GGA TAT  
Pro Pro Thr Asn Ile Ile Met Met Lys Ile Arg Ser Asn Asn Gly Tyr

420 \*

TTTTT AAT TCT TTC CGG TTG TTT ACA TCT TAT AAG ACA AGT TCT TTC  
Phe Asn Ser Phe Arg Leu Phe Thr Ser Tyr Lys Thr Ser Ser Phe Ser  
TCA

**FIGURE 1**  
**1/6**

**FIGURE 1**  
**2/6**

780														
* TTC TTC GAA AAC AGT GTG GTG GAC CAA TTC AAC GAG TGT GCG GTT TCC Leu Phe Glu Asn Ser Val Val Asp Gln Phe Asn Glu Cys Ala Val Ser														
840														
* CGA AAG AAA TGT GTG CCC CGG AAA TCG GAT GTG GGT GAA TTC CCG GTT Arg Lys Lys Cys Val Pro Arg Lys Ser Asp Val Gly Glu Phe Pro Val														
900														
* CCG GAT CGT AAT GCA GTG GTT CAA AAT TTT AAC ATG AAA GAC TTT AGT Pro Asp Arg Asn Ala Val Val Gln Asn Phe Asn Met Lys Asp Phe Ser														
GGG AAG TGG TAT ATA ACA AGT GGT TTA AAT CCT ACA TTT GAT GCA TTT Gly Lys Trp Tyr Ile Thr Ser Gly Leu Asn Pro Thr Phe Asp Ala Phe														
960														
* GAT TGT CAA CTT CAT GAG TTT CAT ATG GAA AAT GAT AAA CTT GTT GGG Asp Cys Gln Leu His Glu Phe His Met Glu Asn Asp Lys Leu Val Gly														
1020														
* AAC TTA ACA TGG CGC ATA AAA ACT TTT GAT GGT GGT TTC TTT ACT CGA Asn Leu Thr Trp Arg Ile Lys Thr Leu Asp Gly Gly Phe Thr Arg														
1080														
* TCT GCT GTG CAA ACA TTT GTT CAA GAT CCA GAT CTT CCT GGA GCA CTT Ser Ala Val Gln Thr Phe Val Gln Asp Pro Asp Leu Pro Gly Ala Leu														

FIGURE 1  
3/6

1140 \*  
TAT AAT CAT GAC AAT GAG TTT CTT CAC TAC CAA GAT GAC TGG TAC ATA  
Tyr Asn His Asp Asn Glu Phe Leu His Tyr Gln Asp Asp Trp Tyr Ile

TTA TCT TCC CAA ATC GAA AAC AAA CCC GAT GAT TAC ATA TTC GTA TAC  
Leu Ser Ser Gln Ile Glu Asn Lys Pro Asp Asp Tyr Ile Phe Val Tyr

1200 \*  
TAC CGA GGT CGA AAC GAC GCA TGG GAT GGA TAC GGT GGG TCC GTG ATC  
Tyr Arg Gly Arg Asn Asp Ala Trp Asp Gly Tyr Gly Ser Val Ile

1260 \*  
TAC ACC CGA AGC CCG ACA CTC CCC GAA TCG ATC ATC CCA AAC CTA CAA  
Tyr Thr Arg Ser Pro Thr Leu Pro Glu Ser Ile Ile Pro Asn Leu Gln

1320 \*  
AAA GCA GCC AAA TCC GTG GGT CGA GAC TTT AAC AAT TTC ATA ACA ACC  
Lys Ala Ala Lys Ser Val Gly Arg Asp Phe Asn Asn Phe Ile Thr Thr

1380 \*  
GAC AAT AGT TGT GGG CCT GAG CCT CCA TTG GTG GAA AGG CTT GAG AAA  
Asp Asn Ser Cys Gly Pro Glu Pro Pro Leu Val Glu Arg Leu Glu Lys

ACA GCG GAA GAG GGC GAG AAG TTG TTG ATA AAA GAA GCT GTA GAG ATA  
Thr Ala Glu Glu Gly Glu Lys Leu Leu Ile Lys Glu Ala Val Glu Ile

FIGURE 1  
4/6

1440  
\*  
GAA GAA GAG GTT GAA AAA GAG GTG GAG AAG GTT AGA GAT ACT GAG ATG  
Glu Glu Glu Val Glu Lys Glu Val Glu Lys Val Arg Asp Thr Glu Met  
1500  
\*  
ACT TTG TTT CAG AGG TTG CTT GAA GGG TTT AAG GAG TTG CAA CAA GAT  
Thr Leu Phe Gln Arg Leu Glu Glu Lys Glu Leu Gln Gln Asp  
1560  
\*  
GAA GAG AAT TTT GTG AGG GAG TTG AGT AAA GAA GAG AAG GAA ATT CTG  
Glu Glu Asn Phe Val Arg Glu Leu Ser Lys Glu Lys Glu Ile Leu  
1620  
\*  
AAT GAA CTT CAA ATG GAA GCG ACT GAA GTT GAA AAG CTT TTT GGG CGC  
Asn Glu Leu Gln Met Glu Ala Thr Glu Val Glu Lys Leu Phe Gly Arg  
1680  
\*  
GCG TTA CCG ATT AGG AAA CTT AGA TAAATTT CGATGATTGA TTCAGACAAT  
Ala Leu Pro Ile Arg Lys Leu Arg  
1740  
\*  
ATATATAGTC ATATGGATTA TGTAGATACT AGAGAAAACC CAAAAAACT TTTGTATACG  
1800  
\*  
TGATAAACGT GTTTGTGATT TGTTTATTGG CTTAAAATTG TAGAATAGCT TTTTAAATTC

**FIGURE 1**  
**5/6**

3434 3434 3434 3434

1860 \*  
TTTACAAAAA AATTGATTGT CTATTGGTAG CCAAGAGGTT CACGAAAAGA CTGAAAGGGT  
1920 \*  
CTTGCCCGGT TTGCGGGTTA GGCCAAATTT TTTGGGGCGG GATCGGTCTT GATCGGGTTT  
1980 \*  
TCTTTAAAA CATGTATTTT TTATAAATGA TGAGTTATTT TCAATTTTTC GCTAAAAAAA

1981  
\*  
A

FIGURE 1  
6/6

[illegible]

56	TATTTTTCATG	AGTTTGCAGT	TGGTGGTAAT	ACGGTTGAAG	A	ATG	GCT	CTT	GCC	CCT						
						Met	Ala	Leu	Ala	Pro						
						1				5						
104	CAT	TCA	AAT	TTT	CTG	GCC	AAC	CAT	GAA	ACC	ATC	AAA	TAT	TAT	GTT	GGG
	His	Ser	Asn	Phe	Leu	Ala	Asn	His	Glu	Thr	Ile	Lys	Tyr	Tyr	Val	Gly
					10				15						20	
152	TCA	AAG	CTT	CCC	GGT	CAT	AAA	AGG	TTT	AGC	TGG	GGT	TGG	GAA	GAT	TAC
	Ser	Lys	Leu	Pro	Gly	His	Lys	Arg	Phe	Ser	Trp	Gly	Trp	Glu	Asp	Tyr
				25					30					35		
200	TTT	GGT	AGT	ATA	GTC	GTA	GCA	AAA	ATT	TGT	TCC	AGC	AGA	CGG	ATA	CCT
	Phe	Gly	Ser	Ile	Val	Val	Ala	Lys	Ile	Cys	Ser	Ser	Arg	Arg	Ile	Pro
			40				45						50			
248	AGA	TAC	TTT	CGA	AAA	TCT	CCT	AGA	ATA	TGC	TGT	GGT	TTG	GAT	TCA	AGA
	Arg	Tyr	Phe	Arg	Lys	Ser	Pro	Arg	Ile	Cys	Cys	Gly	Leu	Asp	Ser	Arg
		55					60					65				
296	GGT	CTG	CAA	CTA	TTC	TCA	CAC	GGG	AAA	CAC	AAT	CTC	TCT	CCC	GCA	CAT
	Gly	Leu	Gln	Leu	Phe	Ser	His	Gly	Lys	His	Asn	Leu	Ser	Pro	Ala	His
		70				75					80					85
344	AGC	ATT	AAC	CAG	AAT	GTA	CCT	AAG	GGA	AAT	TCA	GGA	TGC	AAA	TTT	CCA
	Ser	Ile	Asn	Gln	Asn	Val	Pro	Lys	Gly	Asn	Ser	Gly	Cys	Lys	Phe	Pro
					90					95					100	

FIGURE 2  
1/5

# Sequence alignment

AAA GAT GTA GCT TTG ATG GTT TGG GAG AAA TGG GGC CAA TTT GCC AAA Lys Asp Val Ala Leu Met Val Trp Glu Lys Trp Gly Gln Phe Ala Lys	105 110 115	392
ACA GCA ATT GTA GCT ATA TTC ATT TTG TCA GTT GCT TCA AAA GCT GAT Thr Ala Ile Val Ala Ile Phe Ile Leu Ser Val Ala Ser Lys Ala Asp	120 125	440
GCG GTT GAT GCT CTC AAG ACT TGT ACT TGC TTA CTG AAA GAG TGC AGG Ala Val Asp Ala Leu Lys Thr Cys Thr Cys Leu Leu Lys Glu Cys Arg	135 140	488
TTA GAG CTT GCG AAG TGC ATT TCG AAC CCT GCA TGT GCA GCT AAT GTT Leu Glu Leu Ala Lys Cys Ile Ser Asn Pro Ala Cys Ala Ala Asn Val	150 155	536
GCC TGT CTC CAG ACT TGC AAC AAT AGA CCT GAC GAA ACG GAA TGT CAG Ala Cys Leu Gln Thr Cys Asn Asn Arg Pro Asp Glu Thr Glu Cys Gln	170 175	584
ATA AAA TGT GGT GAT TTG TTT GAA AAC AGT GTC GTA GAC GAG TTC AAT Ile Lys Cys Gly Asp Leu Phe Glu Asn Ser Val Val Asp Glu Phe Asn	185 190	632
GAG TGT GCA GTC TCC CGA AAG AAA TGT GTA CCT CGT AAA TCT GAT GTT Glu Cys Ala Val Ser Arg Lys Lys Cys Val Pro Arg Lys Ser Asp Val	200 205	680

FIGURE 2  
2/5



# Sequence alignment

GGT GAC TTT CCT GTA CCT GAT CCC AGT GTT CTT GTC CAG AAG TTT GAC Gly Asp Phe Pro Val Pro Asp Pro Ser Val Leu Val Gln Lys Phe Asp 215 220 225	728
ATG AAA GAT TTT AGC GGG AAA TGG TTC ATT ACT CGC GGT TTG AAT CCC Met Lys Asp Phe Ser Gly Lys Trp Phe Ile Thr Arg Gly Leu Asn Pro 230 235 240 245	776
ACT TTT GAT GCT TTT GAT TGC CAA TTG CAT GAG TTC CAT ACA GAA GAA Thr Phe Asp Ala Phe Asp Cys Gln Leu His Glu Phe Thr Glu Glu 250 255 260	824
AAC AAA CTT GTG GGG AAT TTA TCT TGG AGA ATA CGT ACA CCT GAT GGA Asn Lys Leu Val Gly Asn Leu Ser Trp Arg Ile Arg Thr Pro Asp Gly 265 270 275	872
GGA TTT TTT ACT CGA TCA GCG GTG CAA AAA TTC GTG CAA GAT CCA AAG Gly Phe Phe Thr Arg Ser Ala Val Gln Lys Phe Val Gln Asp Pro Lys 280 285 290	920
TAT CCG GGG ATA CTC TAC AAT GAT AAT AAT AAT AAT AAT AAT AAT AAT Tyr Pro Gly Ile Leu Tyr Asn His Asp Asn Glu Tyr Leu Leu Tyr Gln 295 300 305	968
GAT GAC TGG TAT ATT TTG TCA TCC AAA GTA GAA AAT AGT CCA GAG GAT Asp Asp Trp Tyr Ile Leu Ser Ser Lys Val Glu Asn Ser Pro Glu Asp 310 315 320 325	1016

FIGURE 2  
3/5

TAC ATA TTT GTG TAC TAT AAG GGC AGA AAT GAT GCA TGG GAT GGA TAT Tyr Ile Phe Val 330 Tyr Tyr 335 Asn Asp Ala Trp Asp Gly Tyr 340	1064
GGT GGT TCT GTA CTT TAC ACA AGA AGT GCA GTT TTG CCT GAA AGC ATT Gly Gly Ser Val 345 Leu Tyr Thr Arg Ser Ala Val Leu Pro Glu Ser Ile 355	1112
ATA CCG GAG TTG CAA ACC GCA GCT CAA AAA GTT GGG CGT GAT TTC AAC Ile Pro Glu Leu 360 Gln Thr Ala Ala 365 Gln Lys Val Gly Arg Asp Phe Asn 370	1160
ACA TTC ATA AAA ACA GAC AAT ACA TGT GGC CCT GAA CCT CCC CTT GTT Thr Phe Ile Lys Thr Asp Asn Thr Cys Gly Pro Glu Pro Pro Leu Val 385	1208
GAG AGG TTG GAG AAG AAA AAG GTG GAA GAA GGA GAA AGG ACG ATC ATA AAA Glu Arg Leu Glu Lys 390 Lys Lys 395 Val Glu Glu Gly 400 Glu Arg Thr Ile Ile Lys 405	1256
GAA GTT GAG GAG ATA GAA GAA GAA GAA GAA GAA GAA GAA GAA GAA GAA Glu Val Glu Glu Ile 410 Glu Glu Glu Val Glu Lys Val Arg Asp Lys Glu 420	1304
GTC ACC TTA TTC AGT AAA CTG TTT GAA GGT TTT AAA GAG CTC CAA CGA Val Thr Leu Phe Ser Lys Leu Phe Glu Glu Lys Lys Glu Leu Gln Arg 435	1352

# Sequence Alignment

GAT GAA GAG AAC TTC TTA AGA GAG CTG AGC AAA GAA GAA ATG GAT GTT	1400
Asp Glu Glu Asn Phe Leu Arg Glu Ser Lys Glu Glu Met Asp Val	
440	450
TTG GAT GGA CTT AAA ATG GAA GCA ACT GAG GTA GAA AAA CTT TTT GGG	1448
Leu Asp Gly Leu Lys Met Glu Ala Thr Glu Val Glu Lys Leu Phe Gly	
455	465
CGT GCT TTA CCA ATA AGG AAA TTA A GGTAAGT ATTTTAAAAA CTATCAACAT	1500
Arg Ala Leu Pro Ile Arg Lys Leu	
470	
ATATACTACA TGTATAGTTG TATTGATTG TTTTGCCTGG AATAGATTGC TTATACATCA	1560
TGTATTGCTT CTTTTTCAGA AGCAAAAAA	1589

56  
Met Ala Val Ala

1

104  
ACA CAT TGT TTC ACT TCA CCT TGT CAT GAC CGT ATT CGA TTT TTC TCA

Thr His Cys Phe Thr Ser Pro Cys His Asp Arg Ile Arg Phe Ser  
5 10 15 20

152  
AGT GAT GAT GGT ATT GGT AGG CTT GGC ATT ACA AGA AAG AGG ATC AAT

Ser Asp Asp Gly Ile Gly Arg Leu Gly Ile Thr Arg Lys Arg Ile Asn  
25 30 35

200  
GGC ACT TTC TTG CTC AAG ATT TTA CCT CCA ATC CAA AGT GCT GAT CTC

Gly Thr Phe Leu Leu Lys Ile Leu Pro Pro Ile Gln Ser Ala Asp Leu  
40 45 50

248  
AGA ACA ACT GGT GGG AGA TCC TCA CGT CCT TTA TCT GCA TTC AGG TCA

Arg Thr Thr Gly Gly Arg Ser Ser Arg Pro Leu Ser Ala Phe Arg Ser  
55 60 65

296  
GGA TTC TCT AAG GGG ATA TTT GAC ATT GTG CCA TTA CCA TCA AAG AAT

Gly Phe Ser Lys Gly Ile Phe Asp Ile Val Pro Leu Pro Ser Lys Asn  
70 75 80

344  
GAG CTG AAA GAG CTG ACC GCT CCG CTG TTG CTA AAA CTC GTG GGT GTT

Glu Leu Lys Glu Leu Thr Ala Pro Leu Leu Lys Leu Val Gly Val  
85 90 95 100

# Sequence alignment

TTA GCT TGC GCG TTC CTT ATT GTT CCA TCT GCA GAT GCA GTT GAT GCA	392
Leu Ala Cys Ala Phe 105	
Leu 110	
Leu 115	
CTT AAA ACT TGT GCA TGC TTA TTG AAG GGA TGC AGG ATA GAA CTC GCA	440
Leu Lys Thr Cys Ala 120	
Leu 125	
Leu 130	
AAG TGC ATT GCC AAC CCT GCC TGT GCA GCC AAT GTC GCG TGC CTT CAG	488
Lys Cys Ile Ala Asn 135	
Lys 140	
Lys 145	
ACC TGC AAT AAC CGT CCA GAT GAA ACC GAG TGC CAG ATT AAA TGT GGG	536
Thr Cys Asn Asn Arg 150	
Thr 155	
Thr 160	
GAT CTG TTT GAG AAC AGT GTT GAT GAG TTC AAC GAG TGT GCT GTG	584
Asp Leu Phe Glu Asn 165	
Asp 170	
Asp 175	
Asp 180	
TCG AGA AAA AAG TGT GTT CCT CCT AGA AAA TCT GAT CTC GGA GAA TTT CCT	632
Ser Arg Lys Lys Cys Val 185	
Ser 190	
Ser 195	
GCC CCA GAC CCT TCT GTT CTT GTA CAG AAC TTC AAC ATC TCG GAC TTT	680
Ala Pro Asp 200	
Ala 205	
Ala 210	

# Sequence

AAC GGG AAG TGG TAC ATT ACA AGT GGC TTG AAT CCA ACC TTT GAT GCC Asn Gly Lys Trp Tyr Ile Thr Ser Gly Leu Asn Pro Thr Phe Asp Ala	728
TTC GAC TGC CAG CTG CAT GAG TTC CAC ACA GAA GGT GAC AAC AAG CTT Phe Asp Cys Gln Leu His Glu Phe His Thr Glu Gly Asp Asn Lys Leu	776
GTT GGA AAC ATC TCT TGG AGA ATA AAG ACC CTA GAC AGT GGA TTC TTT Val Gly Asn Ile Ser Trp Arg Ile Lys Thr Leu Asp Ser Gly Phe Phe	824
ACT AGG TCA GCC GTA CAA AAA TTC GTG CAA GAT CCT AAC CAA CCT GGT Thr Arg Ser Ala Val Gln Lys Phe Val Gln Asp Pro Asn Gln Pro Gly	872
GTT CTC TAC AAT CAT GAC AAC AAG GAG TAC CTT CAC His Tyr Gln Asp Trp Val Leu Tyr Asn His Asn Glu Tyr Leu His Tyr Gln Asp Asp Trp	920
TAT ATC CTG TCA TCA AAG ATA GAG AAT AAA CCT GAA GAC TAT ATA TTT Tyr Ile Leu Ser Ser Ser Lys Ile Glu Asn Lys Pro Glu Asp Tyr Ile Phe	968
GTA TAC TAC CGT GGG CGA AAC AAT GAT GCT TGG GAT GGA TAT GGT GGT GCA Val Tyr Tyr Arg Gly Arg Asn Asp Ala Trp Asp Gly Tyr Gly Gly Ala	1016

FIGURE 3  
3/5

# 362333-362333

GTT GTA TAC ACG AGA AGT TCT GTA TTA CCC AAT AGC ATT ATA CCA GAA 1064  
Val Val Tyr Thr Arg Ser Ser Val Leu Pro Asn Ser Ile Ile Pro Glu 340  
325 330 335

CTC GAA AAA GCA GCA AAA AGC ATA GGC AGA GAC TTC AGC ACA TTC ATT 1112  
Leu Glu Lys Ala Ala Lys Ser Ile Gly Arg Asp Phe Ser Thr Phe Ile 355  
345 350

AGA ACG GAT AAC ACA TGT GGT CCT GAA CCT GCG CTC GTG GAG AGA ATT 1160  
Arg Thr Asp Asn Thr Cys Gly Pro Glu Pro Ala Leu Val Glu Arg Ile 370  
360 365

GAG AAG ACA GTG GAA GAA GGT GAA AGG ATA ATC GTA AAA GAG GTT GAA 1208  
Glu Lys Thr Val Glu Glu Gly Glu Arg Ile Ile Val Lys Glu Val Glu 385  
375 380

GAG ATA GAA GAA GAG GTA GAG AAG GAA GTG GAG AAG GTC GGT AGG ACT 1256  
Glu Ile Glu Glu Glu Val Glu Lys Glu Val Glu Lys Val Gly Arg Thr 400  
390 395

GAG ATG ACC TTG TTC CAG AGA TTG GCT GAA GGA TTT AAT GAA CTG AAG 1304  
Glu Met Thr Leu Phe Gln Arg Leu Ala Glu Gly Phe Asn Glu Leu Lys 420  
405 410 415

CAA GAC GAG GAG AAT TTC GTG AGA GAG TTA AGT AAA GAA GAG ATG GAG 1352  
Gln Asp Glu Glu Asn Phe Val Arg Glu Leu Ser Lys Glu Glu Met Glu 435  
425 430

TTT	TTG	GAT	GAG	ATC	AAA	ATG	GAA	GCA	AGT	GAG	GTT	GAA	AAA	TTG	TTT	1400
Phe	Leu	Asp	Glu	Ile	Lys	Met	Glu	Ala	Ser	Glu	Val	Glu	Lys	Leu	Phe	
			440					445					450			
GGG AAA GCT TTG CCA ATC AGG AAG GTC AGG TAGAAACAAG AACCAACATT																1450
Gly Lys Ala Leu Pro Ile Arg Lys Val Arg																
			455					460								
GTTGTACAAA CTATATTATA CATACTGTGT TCGGTTTCATA TAAAGTAATA TTTTGTGACA																1510
CAGTCATCAT CATTCCATAA CAATTGGATA AAAAAAAAAA AAAAAA																1555

5/5



Tobacco	MALAPHSNFLANHETIKYYVGSGLPGHKRFSWGWEDYFGSIVVAKICSSR	50
Arabidopsis	M-V-T-.....CFT-PCHDRI--FSS.D-GI-RLGITRK....	33
Lettuce	M--SL-TV--CKE-ALNL-AR-PCNE...--HRS.GQPPTN-IMM--....	43
Tobacco	RIPRYFRKSPRICCGLDSEGLQLF.SHGKHNLSPAHSINQNVPKGNSGCK	99
Arabidopsis	--NGT-L..LK-LPPIQ-AD-RTTGGRSSRP--AFR-GFSKGIFDIVPLP	81
Lettuce	-SNNGYFN-F-LFTSYKTSSF..SD-SHCKDK-QI.CSIDTSFEEIQRFD	90
Tobacco	FPKDVALMVWEKVGQFAKTAIVAIFILSVASKADA	134
Arabidopsis	SKNELKELTA...PLLL-LVG-LACAFILVPS---	113
Lettuce	LKRGMT-ILEKQ-R--IQL---LVCTFVIVPRV--	125
Tobacco	VDALKTCTCLLKECRLELAKCISNPACAAVACLQTCNNRPDETECQIKC	50
Arabidopsis	-----A-----G--I-----A-----	50
Lettuce	-----A-----I-----A--S-----	50
Tobacco	GDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVDPDSVLVQKFDMDKDFS	100
Arabidopsis	-----I-E--A-----N-NIS--N	100
Lettuce	-----Q-----E-----RNAV--N-N----	100
Tobacco	GKWFITRGLNPTFDAFDCQLHEFHTE.ENKLVGNLSWRIRTPDGGFFTRS	149
Arabidopsis	---Y--S-----GD-----I---K-L-S-----	150
Lettuce	---Y--S-----M-ND.-----T---K-L-----	149
Tobacco	AVQKFVQDPKYPGILYNHDNEYLLYQDDWYILSSKVENSPEDYIFVYYKG	199
Arabidopsis	-----NQ--V-----H-----I--K-----R-	200
Lettuce	---T---DL--A-----F-H-----QI--K-D-----R-	199
Tobacco	RNDAWDGYGGSVLYTRSAVLPESEIPELQTAAQKVGRDENTFIKTDN*TCG	249
Arabidopsis	-----A-V---S---N-----EK--KSI---S---R-----	250
Lettuce	-----I---PT-----N--K--KS-----N--T---S--	249
Tobacco	PEPPIVERLEKKVEEGERTIIKEVEEIEE...EVEKVRDKEVTLFSKLF	295
Arabidopsis	---A---I---T-----I-V-----EVEK-----GRT-M---QR-A	300
Lettuce	-----TA---KLL---AV---EVEK-----T-M---QR-L	299
Tobacco	EGFKEIQRDEENFLRELSKEEMDVL.DGLKMEATEVEKLFGRALPIRKLK	344
Arabidopsis	---N--KQ---V-----EF--EI---S-----K-----V-	349
Lettuce	-----Q---V-----KEI-NE-Q-----	348



A Cysteine-rich domain

B Lipocalin signature

C Highly charged domain

FIGURE 4

# Percent Identity and Similarity\* of Pre-protein VDE

	Lettuce	Tobacco	Arabidopsis
Lettuce		67 (78)	69 (82)
Tobacco	69	protein cDNA	68 (81)
Arabidopsis	66		68

\*similarity values are in parentheses

# Percent Identity and Similarity\* of Mature VDE

	Lettuce	Tobacco	Arabidopsis
Lettuce		82 (90)	83 (91)
Tobacco	76	protein cDNA	83 (92)
Arabidopsis	74		77

\*similarity values are in parentheses

FIGURE 5

The figure consists of three vertically stacked line graphs, each representing the Hydropathy Index for a different species: Arabidopsis (top), Lettuce (middle), and Tobacco (bottom). The y-axis for all three graphs is labeled 'Hydropathy Index' and ranges from -2 to 3. The x-axis is labeled 'Amino Acid' and ranges from 0 to 140. Each graph shows a fluctuating line representing the hydropathy index across the 140 amino acids. Arabidopsis shows a significant peak around amino acid 125. Lettuce and Tobacco show similar patterns with peaks around amino acid 125 and troughs around amino acid 40.

FIGURE 6

1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385</
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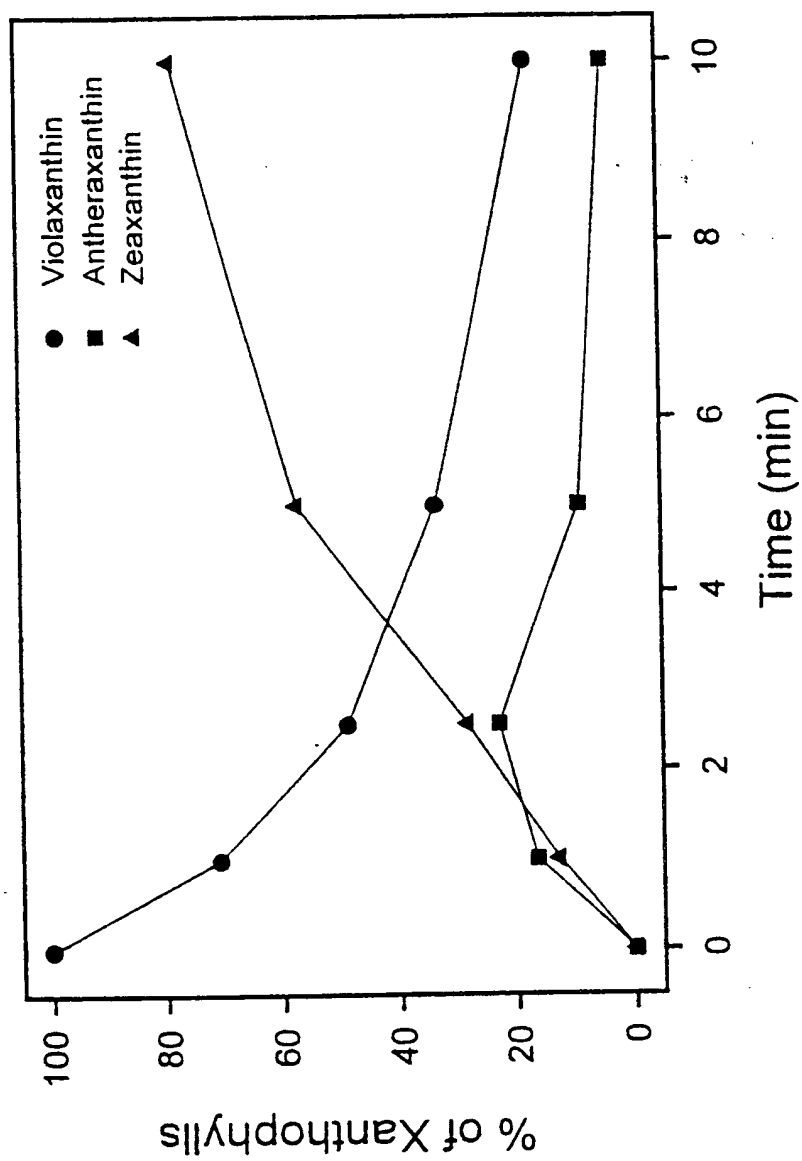


FIGURE 7A

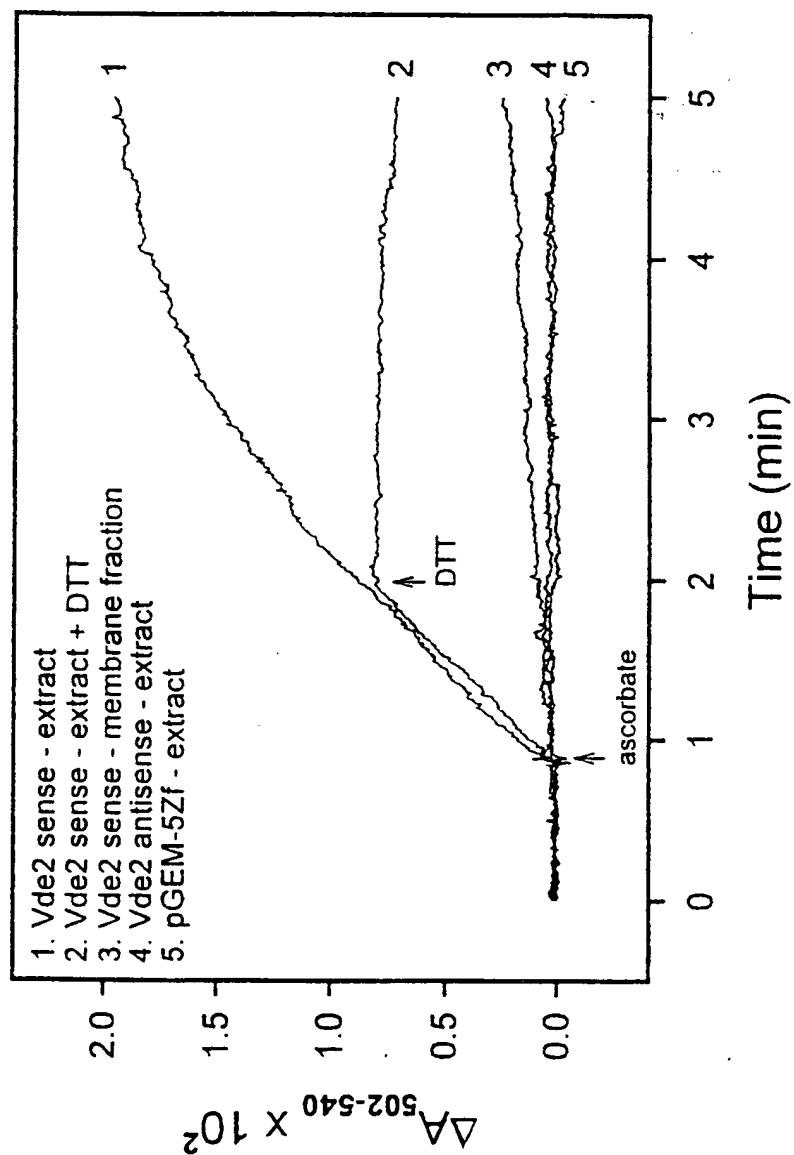
[illegible]

FIGURE 7B

Plant	Treatment	N	V	A	Z	V+A+Z	L	Chlb/Chla	$\beta\beta$ -Carotene	%V Deepoxidized
Cl-11	Dark	77.13	64.67	1.54	0	66.21	335.12	0.39	136.95	
	Light	77.65	25.56	6.25	30.93	62.74	338.15	0.40	131.76	60.5
Cl-14	Dark	71.60	77.74	1.19	0	78.93	312.05	0.36	150.08	
	Light	72.00	29.07	7.97	43.07	80.11	311.36	0.37	151.50	62.6
Cl-15	Dark	76.68	67.44	0	0	67.44	345.73	0.43	130.05	
	Light	74.45	26.73	7.78	37.44	71.95	337.87	0.42	126.36	60.4
Cl-18	Dark	68.28	82.55	2.33	0	84.88	298.36	0.35	136.67	
	Light	69.65	34.50	13.25	38.44	86.19	311.07	0.36	138.95	58.2
Cl-20	Dark	78.45	70.60	2.85	0	73.45	351.57	0.39	139.58	
	Light	77.38	23.14	5.46	42.66	71.26	343.25	0.39	133.61	67.2
Cl-22	Dark	72.68	104.14	3.40	0	107.54	323.93	0.37	138.29	
	Light	72.13	27.63	6.62	78.66	112.91	315.07	0.40	128.30	73.5
Cl-24	Dark	70.77	76.82	1.55	0	78.37	334.20	0.43	132.95	
	Light	76.52	29.35	7.92	45.24	82.51	339.60	0.44	131.55	61.8
Cl-26	Dark	75.28	63.41	0	0	63.41	346.45	0.44	130.38	
	Light	77.34	26.27	6.16	34.19	66.62	346.91	0.44	128.27	58.6
Cl-30	Dark	78.23	59.66	1.73	0	61.39	357.63	0.45	127.62	
	Light	79.37	26.47	4.93	31.61	63.01	352.39	0.46	124.80	55.6
Cl-31	Dark	71.72	75.91	1.74	0	77.65	315.40	0.37	144.24	
	Light	73.00	31.43	8.74	37.65	77.82	312.80	0.38	145.13	58.6
Cl-39	Dark	75.99	77.93	0	0	77.93	335.79	0.43	127.17	
	Light	74.79	26.28	8.07	41.30	75.65	331.35	0.42	123.11	66.3
Cl-40	Dark	77.56	79.07	2.99	0	82.06	358.33	0.44	126.05	
	Light	77.78	27.44	10.10	47.92	85.46	352.66	0.43	120.89	65.3

Mean = 62.4 ± 5.0

N = 9'-cis-neoxanthin V = violaxanthin A = antheraxanthin Z = zeaxanthin L = lutein Chla = chlorophyll a Chlb = chlorophyll b  
All values are relative to chlorophyll a (mmol mol<sup>-1</sup> Chla) except Chlb/Chla which is (mol/mol).

FIGURE 8  
1 OF 3

Plant	Treatment	N	V	A	Z	V+A+Z	L	Chlb/Chla	ββ-Carotene	%V De-epoxidized	% Inhibition of De-epoxidation
TAS-32	Dark	74.19	76.98	0	0	76.98	325.75	0.42	136.45		94.1
	Light	73.78	74.15	2.18	0	76.33	330.95	0.41	131.73	3.7	
TAS-39	Dark	77.92	59.19	0	0	59.19	329.29	0.41	141.45		92.5
	Light	75.06	56.39	2.70	0	59.09	322.29	0.40	141.52	4.7	
TAS-21	Dark	75.78	53.19	0	0	53.19	335.21	0.45	132.85		72.0
	Light	77.92	43.90	7.30	9.37	60.57	326.90	0.45	130.33	17.5	
TAS-5	Dark	67.82	79.21	3.43	0	82.64	300.82	0.39	139.00		65.9
	Light	69.72	62.31	14.66	8.27	85.24	300.63	0.40	137.13	21.3	
TAS-17	Dark	74.89	64.54	1.08	0	65.62	317.69	0.41	143.42		63.6
	Light	74.00	49.89	8.49	8.53	66.91	325.32	0.40	139.28	22.7	
TAS-13	Dark	77.92	49.33	1.27	0	50.60	339.63	0.45	135.36		62.7
	Light	78.02	37.82	4.94	7.18	49.94	340.45	0.45	132.78	23.3	
TAS-6	Dark	74.42	55.77	0	0	55.77	340.84	0.44	136.77		55.4
	Light	74.95	40.27	9.69	13.99	63.95	332.00	0.44	135.36	27.8	
TAS-37	Dark	73.05	59.18	1.24	0	60.42	323.30	0.39	135.81		45.3
	Light	71.36	38.97	14.48	9.98	63.43	313.46	0.38	134.62	34.1	
TAS-3	Dark	74.04	60.25	1.76	0	62.01	319.39	0.43	138.89		44.2
	Light	76.98	39.26	7.41	14.33	61.00	322.14	0.44	136.00	34.8	
TAS-36	Dark	69.77	77.86	1.42	0	79.28	295.52	0.36	151.33		40.1
	Light	70.74	48.73	12.76	12.81	74.30	308.06	0.36	151.35	37.4	
TAS-35	Dark	75.59	63.24	1.05	0	64.29	342.09	0.42	130.30		39.7
	Light	75.76	39.48	10.38	17.49	67.35	337.57	0.42	128.88	37.6	
TAS-4	Dark	73.61	68.23	1.31	0	69.54	321.12	0.42	135.43		38.6
	Light	73.23	42.07	8.95	17.84	68.86	320.33	0.42	131.73	38.3	
TAS-9	Dark	72.28	52.57	1.75	0	54.32	324.02	0.42	140.21		36.4
	Light	73.28	31.72	6.19	18.59	56.50	317.11	0.42	136.93	39.7	
TAS-7	Dark	72.55	71.02	1.81	0	72.83	321.37	0.40	133.21		

FIGURE 8  
N OF 3

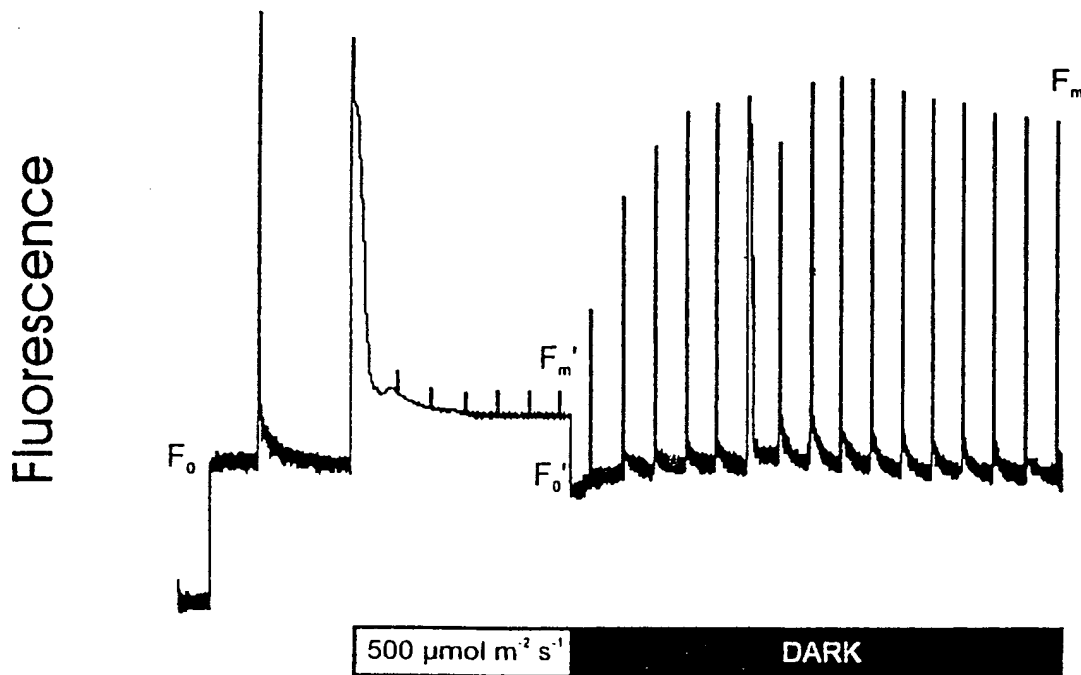
	Light	71.79	39.82	14.04	21.09	74.95	322.04	0.40	130.57	43.9	29.6
TAS-38	Dark	71.66	61.97	1.77	0	63.74	329.67	0.41	135.87		
	Light	73.24	34.45	8.83	19.57	62.85	331.17	0.41	133.77	44.4	28.8
TAS-16	Dark	72.15	62.54	2.04	0	64.58	329.72	0.41	135.12		
	Light	74.04	33.28	9.10	23.83	66.21	335.60	0.42	131.32	46.8	25.0
TAS-18	Dark	75.09	59.64	1.72	0	61.36	345.04	0.42	127.38		
	Light	75.26	31.68	7.11	23.01	61.80	340.79	0.42	126.85	46.9	24.8
TAS-34	Dark	72.35	65.39	1.79	0	67.18	326.06	0.41	131.12		
	Light	71.25	34.26	9.26	30.41	73.93	316.49	0.42	128.96	47.6	23.7

N = 9'-cis-neoxanthin V = violaxanthin A = antheraxanthin Z = zeaxanthin L = lutein Chla = chlorophyll a Chlb = chlorophyll b

All values are relative to chlorophyll a (mmol mol<sup>-1</sup> Chla) except Chlb/Chla which is (mol/mol).



Ct-30

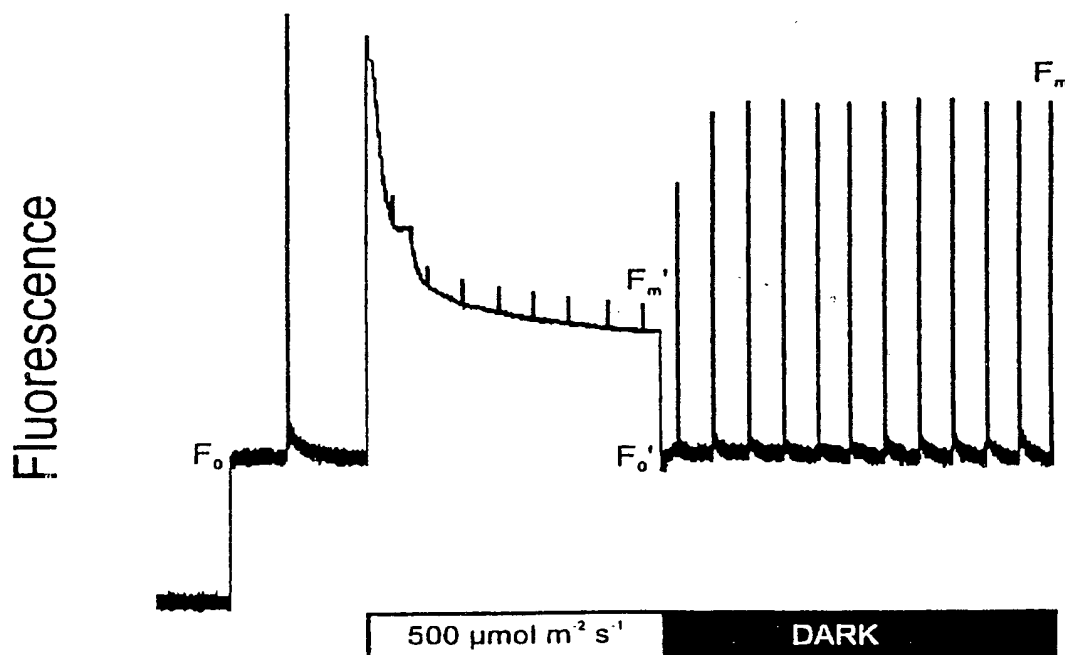


	Dark-adapted	Pre-illuminated	Post-fluorescence Analysis
V	64.28	51.77	44.98
A	1.99	6.16	11.10
Z	0	10.17	13.77
V+A+Z	66.27	68.10	69.85
De-epoxidation (%)		19.5	30.00
(Fm/Fm') - 1			2.20
(Fo/Fo') - 1			0.15

All values are relative to chlorophyll a ( $\text{mmol mol}^{-1} \text{Chla}$ ).

FIGURE 9

# TAS-5



	Dark-adapted	Pre-illuminated	Post-fluorescence Analysis
V	67.51	NA	65.38
A	0	NA	2.14
Z	0	NA	0
V+A+Z	67.51	NA	67.52
De-epoxidation (%)		NA	3.20
(Fm/Fm') - 1			1.34
(Fo/Fo') - 1			0

All values are relative to chlorophyll a ( $\text{mmol mol}^{-1} \text{Chla}$ ).

NA - Not assayed

FIGURE 10